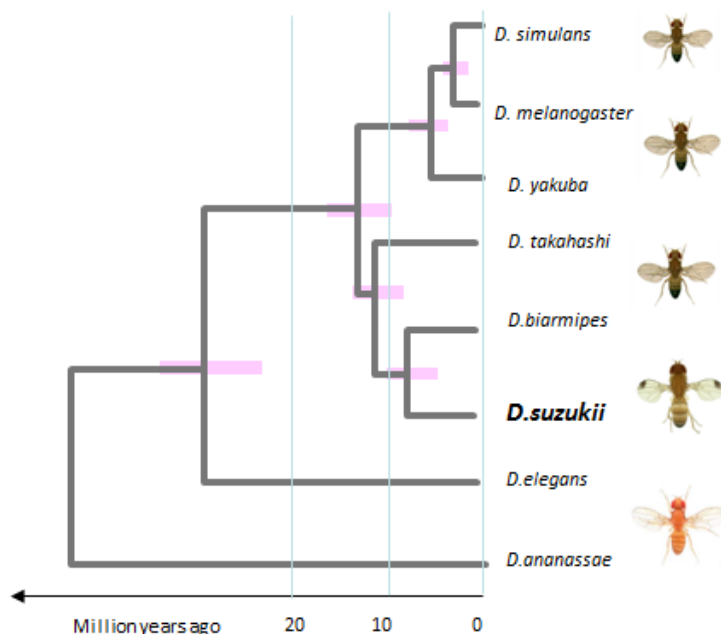


## Sibe Crash Course in Phylogenetics

(limited space for enrollment)



The Italian Society for Evolutionary Biology (SIBE-ISEB)

is offering a crash course in Molecular Phylogenetics to be held in Rome August 28<sup>th</sup> 2017.

The course is aimed at students and young researchers interested in taking their first steps into the fabulous world of Phylogenetics, or to those who want to refresh it. The course is free, but only for members of the SIBE who will attend the Evoluzione2017 SIBE's congress in Rome (you can join the society starting from 15Euro at at <http://www.sibe-iseb.it/subscribe-to-iseb/s87d97886> and register for the congress from 60 Euro at <http://sibe2017.uniroma2.it/registration>). Registration is on a first come first served basis; participants should send a short motivation letter, and proof of registration to the meeting to [omar.rota@fmach.it](mailto:omar.rota@fmach.it) before August 1; acceptance will be notified shortly after.

Course consists of 4 sessions of an hour each. Lectures (40 minutes) will cover the basic principles of molecular phylogeny and will be followed by a short tutorial (20 minutes) where the students will analyze a data set provided by teachers (or a small one brought by them). Participants need to bring their own laptop with with 3 programs previously installed: MEGA7 (<http://www.megasoftware.net/>), the BEASTv1.8 package (<http://beast.bio.ed.ac.uk/downloads>) and TRACER (<http://beast.bio.ed.ac.uk/tracer>). Teachers are Omar Rota-Stabelli (Mach Foundation, Trento) and Andrea Luchetti (Bologna University). Course is in English.

### PROGRAM:

9:00 Gathering and softwares check.

**9: 30-10.30 The Genesis: In the beginning the selection created the ortholog and the paralog.** A brief introduction to phylogenetic markers, design of a phylogenetic analysis, the concept of orthology, retrieving orthologous sequences from databases or their amplification from DNA, the data type, nucleotide versus amino acids, the progressive and iterative alignment. Hand-on training of MEGA.

**10:30-11.30 The Phylogentic Trinity: Distance, Parsimony, Likelihood.** Anatomy of a phylogenetic tree, genetic distances and Neighbor-Joining, substitution models and among sites rate variation, Maximum Parsimony and Maximum

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Likelihood.

11:30 to 12:00 Coffee break

**12: 00- 13:00 The Bayesian Reform and the Revelation of time.** Bayesian inference, the MCMC, convergence, harvest and burn-in, model selection with Bayes factor, estimating the temporal divergence in a phylogeny, priors and calibrations. Hand-on with BEAST and Tracer.

**13:00 to 13:30 Mortal sins and final confession.** A final synthesis with a focus on the most common mistakes do phylogeny. Questions and discussion.

### **WHERE AND WHEN**

**Università degli studi “Roma Tre”**

Dipartimento di Scienze - Viale G. Marconi, 446 Rome

**Monday, August 28 9:00 am**